

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Atty. Docket No: 078003-0280681

In re patent application of  
ADLER, JON ELLIOT et al.

Serial No. 10/035,045

Filed: January 3, 2002

For: T1R TASTE RECEPTORS AND GENES ENCODING SAME



STATEMENT TO SUPPORT FILING AND SUBMISSION IN  
ACCORDANCE WITH 37 C.F.R. §§ 1.821-1.825

Assistant Commissioner for Patents  
Washington, D.C. 20231  
**Box SEQUENCE**

Sir:

In connection with a Sequence Listing submitted concurrently herewith, the undersigned hereby states that:

1. the submission, filed herewith in accordance with 37 C.F.R. § 1.821(g), does not include new matter;

2. the content of the attached paper copy and the attached computer readable copy of the Sequence Listing, submitted in accordance with 37 C.F.R. § 1.821(c) and (e), respectively, are the same; and

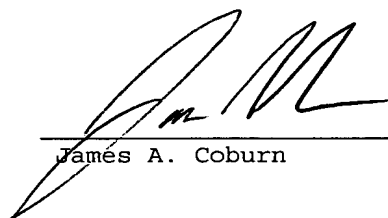
3. all statements made herein of their own knowledge are true and that all statements made on information and belief are believed to be true; and further, that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under Section 1001 of Title 18 of the United

Serial No. 10/035,045

States Code and that such willful false statements may jeopardize the validity of the application or any patent resulting therefrom.

Respectfully submitted,

March 25, 2002  
Date

  
James A. Coburn

**HARBOR CONSULTING**  
Intellectual Property Services  
1500A Lafayette Road  
Suite 262  
Portsmouth, N.H.  
800-318-3021



## SEQUENCE LISTING

<110> ADLER, JON ELLIOT  
LI, XIAODONG  
STASZEWSKI, LENA  
O'CONNELL, SHAWN  
ZOZULYA, SERGEY

<120> T1R TASTE RECEPTORS AND GENES ENCODING SAME

<130> 078003-0280681

<140> 10/035,045

<141> 2002-01-03

<150> 60/259,227

<151> 2001-01-03

<150> 60/284,547

<151> 2001-04-19

<160> 24

<170> PatentIn Ver. 2.1

<210> 1

<211> 876

<212> DNA

<213> Homo sapiens

<400> 1

```
agcctggcag tggcctcagg cagagtctga cgcgcacaaa ctttcaggcc caggaagcga 60
ggacaccact ggggccccag ggtgtggcaa gtgaggatgg caagggtttt gctaaacaaa 120
tcctctgccc gctccccgcc ccgggctcac tccatgtgag gccccagtcg gggcagccac 180
ctgccgtgcc tgttgggaagt tgcctctgcc atgctggggc ctgctgtcct gggcctcagc 240
ctctgggctc tcctgcaccc tgggacgggg gccccattgt gcctgtcaca gcaacttagg 300
atgaaggggg actacgtgct gggggggctg ttccccctgg gcgaggccga ggaggctggc 360
ctccgcagcc ggacacggcc cagcagccct gtgtgcacca ggtacagagg tgggacggcc 420
tgggtcgggg tcagggtgac caggtctggg gtgctcctga gctggggccg aggtggccat 480
ctgcggttct gtgtggcccc aggttctcct caaacggcct gctctgggca ctggccatga 540
aaatggccgt ggaggagatc aacaacaagt cggatctgct gcccgggctg cgcctgggct 600
acgacctctt tgatacgtgc tcggagcctg tggtagccat gaagcccagc ctcatgttcc 660
tggccaaggc aggcagccgc gacatcgccc cctactgcaa ctacacgcag taccagcccc 720
gtgtgctggc tgtcatcggg cccactcgt cagagctcgc catggtcacc ggcaagttct 780
tcagcttctt cctcatgccc cagtggggcg cccccacca tcaccaccc ccaaccaacc 840
cctgccccgt gggagccctt tgtgtcagga gaatgc 876
```

<210> 2

<211> 2687

<212> DNA

<213> Homo sapiens

<400> 2

```
tacatgcacc ccaccagcc ctgccctggg agccctgtgt cagaagatgc tcttggcctt 60
gcaggtcagc tacgggtgta gcatggagct gctgagcgcc cgggagacct tccccctctt 120
cttccgcacc gtgcccagcg accgtgtgca gctgacggcc gccgcggagc tgctgcagga 180
gttcggctgg aactgggtgg ccgccctggg cagcgacgac gactacggcc ggcagggcct 240
```

```

gagcatcttc tggccctgg ccgcgccacg cggcatctgc atcgcgacg agggcctggt 300
gccgtgccc cgtgccgatg actcgcggtt ggggaagggt caggacgtcc tgcaccaggt 360
gaaccagagc agcgtgcagg tgggtgctgt gttcgctcc gtgcacgccg cccacgccct 420
cttcaactac agcatcagca gcaggctctc gcccaagggt tgggtggcca gcgaggcctg 480
gctgacctct gacctggtca tggggctgcc cggcatggcc cagatgggca cgggtgcttg 540
cttctccag aggggtgcc agctgcacga gttccccag tacgtgaaga cgcacctggc 600
cctggccacc gaccggcct tctgctctgc cctggcgag agggagcagg gtctggagga 660
ggacgtggtg ggccagcgt gcccgagtg tgactgcac acgctgcaga acgtgagcgc 720
agggctaaat caccaccaga cgttctctgt ctacgcagct gtgtatagcg tggcccaggc 780
cctgcacaac actcttcagt gcaacgcctc aggtgcccc gcgcaggacc ccgtgaagcc 840
ctggcagggt agcccgagg atgggggtgt gctgtcctct gcatgtgccc aggccaccag 900
gcacggccac cacgcctgag ctggagggtg ctggcggtc agccccgtcc cccgcccgca 960
gctcctggag aacatgtaca acctgacctt ccacgtgggc gggctgccgc tgcggttcga 1020
cagcagcaga aacgtggaca tggagtacga cctggaagct tgggtgtggc agggctcagt 1080
gcccaggctc cacgacgtgg gcaggttcaa cggcagcctc aggcagagac gcctgaagat 1140
ccgctggcac acgtctgaca accaggtgag gtgaggggtg gtgtgccagg cgtgcccgct 1200
gtagcccccg cggcagggcg cagcctgggg gtggggggcg ttccagtctc ccgtgggcat 1260
gcccagccga gcagagccag accccaggcc tgtgcgcaga agcccggtc ccggtgctcg 1320
cggcagtgcc aggggggcca ggtgcgcgg gtcaagggtt tccactcctg ctgctacgac 1380
tgtgtggact gcagggcggg cagctaccgg caaaaccag gtgagccgcc ttccggcag 1440
gcgggggtgg gaacgcagca ggggagggtc ctgccaagtc ctgactctga gaccagagcc 1500
cacagggtac aagacgaaca cccagcgccc ttctcctctc tcacagacga catcgccctg 1560
accttttgtg gccaggatga gtggtccccg gagcgaagca cacgtgctt ccgccgcagg 1620
tctcggttcc tggcatgggg cgagccggct gtgctgctgc tgcctcctgt gctgagcctg 1680
gcgctggggc ttgtgctggc tgccttgggg ctgttcgttc accatcgggg cagccactg 1740
gttcaggcct cggggggggc cctggcctgc tttggcctgg tgtgcctggg cctggtctgc 1800
ctcagcgtec tctgttccc tggccagccc agccctgccc gatgcctggc ccagagccc 1860
ttgtcccacc tcccgtcac gggctgcctg agcacactct tctgcaggc ggccgagatc 1920
ttcgtggagt cagaactgcc tctgagctgg gcagaccggc tgagtggctg cctgcggggg 1980
ccctgggcct ggctggtggt gctgctggcc atgctggtgg aggtcgact gtgcacctg 2040
tacctggtgg ccttcccggc ggaggtggtg acggactggc acatgctgcc cacggaggcg 2100
ctggtgcact gccgcacacg ctctgggtc agcttcgggc tagcgcacgc caccaatgcc 2160
acgctggcct ttctctgctt cctgggcact ttctggtgc ggagccagcc gggctgctac 2220
aaccgtgccc gtggcctcac ctttgccatg ctggcctact tcacacctg ggtctcctt 2280
gtgcccctcc tggccaatgt gcaggtggtc ctacaggccc ccgtgcagat gggcgccctc 2340
ctgctctgtg tctgggcat cctggctgcc ttccacctgc ccaggtgtta cctgctcatg 2400
cggcagccag ggctcaacac ccccgagttc ttctgggag ggggccctgg ggatgccc 2460
ggccagaatg acgggaacac aggaatcag gggaaacatg agtgaccaa ccctgtgatc 2520
tcagcccgg tgaaccaga cttagctgcg atcccccca agccagcaat gaccgtgtc 2580
tcgctacaga gacctcccg ctctaggttc tgaccccagg ttgtctcctg acctgacct 2640
cacagtgagc cctaggcctg gagcacgtgg acaccctgt gaccatc 2687

```

<210> 3

<211> 2559

<212> DNA

<213> Homo sapiens

<400> 3

```

atgctggggc ctgctgtcct gggcctcagc ctctgggctc tctgcaccc tgggacgggg 60
gccccattgt gcctgtcaca gcaacttagg atgaaggggg actacgtgct gggggggctg 120
ttccccctgg gcgaggccga ggaggctggc ctccgcagcc ggacacggcc cagcagccct 180
gtgtgcacca ggttctcctc aaacggcctg ctctgggcac tggccatgaa aatggccgtg 240
gaggagatca acaacaagtc ggatctgctg cccgggctgc gcctgggcta cgacctctt 300
gatactgtgt cggagcctgt ggtggccatg aagcccagcc tcatgttctt ggccaaggca 360
ggcagccgcg acatcgccgc ctactgcaac tacacgcagt accagccccg tgtgctggct 420
gtcatcgggc cccactcgtc agagctcgcc atgggtcacc gcaagttctt cagcttcttc 480
ctcatgcccc aggtcagcta cggctgctagc atggagctgc tgagcgcccc ggagaccttc 540

```

```

ccctccttct tccgcaccgt gccagcgac cgtgtgcagc tgaaggccgc cgggagctg 600
ctgcaggagt tgggctggaa ctgggtggcc gccctgggca gcgacgacga gtacggccgg 660
cagggcctga gcattcttct ggccctggcc gcggcagcgc gcattctgat cgcgcacgag 720
ggcctgggtgc cgtgcccccg tgccgatgac tcgaggctgg ggaagggtgca ggacgtcctg 780
caccaggtga accagagcag cgtgcagggt gtgctgctgt tcgcctccgt gcacgccgcc 840
cacgcctct tcaactacag catcagcagc aggtctctgc ccaagggtgt ggtggccagc 900
gaggcctggc tgacctctga cctgggtcat gggctgcccc gcattggcca gatgggcacg 960
gtgcttggct tcctccagag gggtgccag ctgcacgagt tccccagta cgtgaagacg 1020
cacctggccc tggccaccga cccggccttc tgctctgccc tgggcgagag ggagcagggt 1080
ctggaggagg acgtggtggg ccagcgctgc ccgagtggt actgcatcac gctgcagaac 1140
gtgagcgagc ggctaaatca ccaccagacg ttctctgtct acgcagctgt gtatagcgtg 1200
gcccaggccc tgcacaacac tcttcagtgc aacgcctcag gctgccccgc gcaggacccc 1260
gtgaagccct ggcagctcct ggagaacatg tacaacctga ccttccacgt gggcgggctg 1320
ccgctcggtg tgacagcagc cggaacatg gacatggagt acgacctgaa gctgtgggtg 1380
tggcagggct cagtggccag gctccacgac gtgggcaggt tcaacggcag cctcaggaca 1440
gagcgctga agatccgctg gcacacgtct gacaaccaga agcccgctgc ccggtgctcg 1500
cggcagtgcc agggaggcca ggtgcgccgg gtcaaggggt tccactcctg ctgctacgac 1560
tgtgtggact gcgaggcggg cagctaccgg caaaacccag acgacatcgc ctgcacctt 1620
tgtggccagg atgagtggtc cccggagcga agcacacgct gcttccgcgc caggtctcgg 1680
ttcctggcat ggggcgagcc ggctgtgctg ctgctgctcc tgctgctgag cctggcgctg 1740
ggccttgctg tggctcctt ggggctgttc gtaccacatc gggacagccc actggttcag 1800
gcctcggggg gggccctggc ctgcttggc ctggtgtgcc tgggcctggt ctgcctcagc 1860
gtcctcctgt tccctggcca gccagccct gcccgatgcc tggcccagca gcccttgtcc 1920
cacctccgc tcacgggctg cctgagcaca ctcttctgc aggcggccga gatcttcgtg 1980
gagtcagaac tgctctgag ctgggcagac cggctgagtg gctgcctgcg ggggccctgg 2040
gcctggctgg tgggtgctgt ggccatgctg gtggagggtc cactgtgcac ctggtacctg 2100
gtggccttcc cgccggagggt ggtgacggac tggcacatgc tggccacgga ggcgctgggt 2160
cactgccga cagctcctg ggtcagcttc ggctagcgc acgccaccaa tgccacgctg 2220
gcctttctct gcttctcggg cactttcctg gtgcggagcc agccgggctg ctacaacctg 2280
gcccgtggcc tcacctttgc catgctggcc tacttcatca cctgggtctc ctttgtgccc 2340
ctcctggcca atgtgcagggt ggtcctcagg cccgccgtgc agatgggcgc cctcctgctc 2400
tgtgtcctgg gcattcctgg tgcttccac ctgcccagggt gttacctgct catgcggcag 2460
ccagggtca acacccccga gttcttctg ggagggggcc ctggggatgc ccaaggccag 2520
aatgacggga acacaggaaa tcaggggaaa catgagtga 2559

```

<210> 4

<211> 852

<212> PRT

<213> Homo sapiens

<400> 4

Met Leu Gly Pro Ala Val Leu Gly Leu Ser Leu Trp Ala Leu Leu His  
1 5 10 15

Pro Gly Thr Gly Ala Pro Leu Cys Leu Ser Gln Gln Leu Arg Met Lys  
20 25 30

Gly Asp Tyr Val Leu Gly Gly Leu Phe Pro Leu Gly Glu Ala Glu Glu  
35 40 45

Ala Gly Leu Arg Ser Arg Thr Arg Pro Ser Ser Pro Val Cys Thr Arg  
50 55 60

Phe Ser Ser Asn Gly Leu Leu Trp Ala Leu Ala Met Lys Met Ala Val  
65 70 75 80

Glu	Glu	Ile	Asn	Asn	Lys	Ser	Asp	Leu	Leu	Pro	Gly	Leu	Arg	Leu	Gly	
				85					90					95		
Tyr	Asp	Leu	Phe	Asp	Thr	Cys	Ser	Glu	Pro	Val	Val	Ala	Met	Lys	Pro	
				100					105					110		
Ser	Leu	Met	Phe	Leu	Ala	Lys	Ala	Gly	Ser	Arg	Asp	Ile	Ala	Ala	Tyr	
				115					120					125		
Cys	Asn	Tyr	Thr	Gln	Tyr	Gln	Pro	Arg	Val	Leu	Ala	Val	Ile	Gly	Pro	
				130					135					140		
His	Ser	Ser	Glu	Leu	Ala	Met	Val	Thr	Gly	Lys	Phe	Phe	Ser	Phe	Phe	
				145					150					155		
Leu	Met	Pro	Gln	Val	Ser	Tyr	Gly	Ala	Ser	Met	Glu	Leu	Leu	Ser	Ala	
				165					170					175		
Arg	Glu	Thr	Phe	Pro	Ser	Phe	Phe	Arg	Thr	Val	Pro	Ser	Asp	Arg	Val	
				180					185					190		
Gln	Leu	Thr	Ala	Ala	Ala	Glu	Leu	Leu	Gln	Glu	Phe	Gly	Trp	Asn	Trp	
				195					200					205		
Val	Ala	Ala	Leu	Gly	Ser	Asp	Asp	Glu	Tyr	Gly	Arg	Gln	Gly	Leu	Ser	
				210					215					220		
Ile	Phe	Ser	Ala	Leu	Ala	Ala	Ala	Arg	Gly	Ile	Cys	Ile	Ala	His	Glu	
				225					230					235		
Gly	Leu	Val	Pro	Leu	Pro	Arg	Ala	Asp	Asp	Ser	Arg	Leu	Gly	Lys	Val	
				245					250					255		
Gln	Asp	Val	Leu	His	Gln	Val	Asn	Gln	Ser	Ser	Val	Gln	Val	Val	Leu	
				260					265					270		
Leu	Phe	Ala	Ser	Val	His	Ala	Ala	His	Ala	Leu	Phe	Asn	Tyr	Ser	Ile	
				275					280					285		
Ser	Ser	Arg	Leu	Ser	Pro	Lys	Val	Trp	Val	Ala	Ser	Glu	Ala	Trp	Leu	
				290					295					300		
Thr	Ser	Asp	Leu	Val	Met	Gly	Leu	Pro	Gly	Met	Ala	Gln	Met	Gly	Thr	
				305					310					315		
Val	Leu	Gly	Phe	Leu	Gln	Arg	Gly	Ala	Gln	Leu	His	Glu	Phe	Pro	Gln	
				325					330					335		
Tyr	Val	Lys	Thr	His	Leu	Ala	Leu	Ala	Thr	Asp	Pro	Ala	Phe	Cys	Ser	
				340					345					350		
Ala	Leu	Gly	Glu	Arg	Glu	Gln	Gly	Leu	Glu	Glu	Asp	Val	Val	Gly	Gln	
				355					360					365		
Arg	Cys	Pro	Gln	Cys	Asp	Cys	Ile	Thr	Leu	Gln	Asn	Val	Ser	Ala	Gly	
				370					375					380		

Leu Asn His His Gln Thr Phe Ser Val Tyr Ala Ala Val Tyr Ser Val  
 385 390 395 400  
 Ala Gln Ala Leu His Asn Thr Leu Gln Cys Asn Ala Ser Gly Cys Pro  
 405 410 415  
 Ala Gln Asp Pro Val Lys Pro Trp Gln Leu Leu Glu Asn Met Tyr Asn  
 420 425 430  
 Leu Thr Phe His Val Gly Gly Leu Pro Leu Arg Phe Asp Ser Ser Gly  
 435 440 445  
 Asn Val Asp Met Glu Tyr Asp Leu Lys Leu Trp Val Trp Gln Gly Ser  
 450 455 460  
 Val Pro Arg Leu His Asp Val Gly Arg Phe Asn Gly Ser Leu Arg Thr  
 465 470 475 480  
 Glu Arg Leu Lys Ile Arg Trp His Thr Ser Asp Asn Gln Lys Pro Val  
 485 490 495  
 Ser Arg Cys Ser Arg Gln Cys Gln Glu Gly Gln Val Arg Arg Val Lys  
 500 505 510  
 Gly Phe His Ser Cys Cys Tyr Asp Cys Val Asp Cys Glu Ala Gly Ser  
 515 520 525  
 Tyr Arg Gln Asn Pro Asp Asp Ile Ala Cys Thr Phe Cys Gly Gln Asp  
 530 535 540  
 Glu Trp Ser Pro Glu Arg Ser Thr Arg Cys Phe Arg Arg Arg Ser Arg  
 545 550 555 560  
 Phe Leu Ala Trp Gly Glu Pro Ala Val Leu Leu Leu Leu Leu Leu  
 565 570 575  
 Ser Leu Ala Leu Gly Leu Val Leu Ala Ala Leu Gly Leu Phe Val His  
 580 585 590  
 His Arg Asp Ser Pro Leu Val Gln Ala Ser Gly Gly Pro Leu Ala Cys  
 595 600 605  
 Phe Gly Leu Val Cys Leu Gly Leu Val Cys Leu Ser Val Leu Leu Phe  
 610 615 620  
 Pro Gly Gln Pro Ser Pro Ala Arg Cys Leu Ala Gln Gln Pro Leu Ser  
 625 630 635 640  
 His Leu Pro Leu Thr Gly Cys Leu Ser Thr Leu Phe Leu Gln Ala Ala  
 645 650 655  
 Glu Ile Phe Val Glu Ser Glu Leu Pro Leu Ser Trp Ala Asp Arg Leu  
 660 665 670  
 Ser Gly Cys Leu Arg Gly Pro Trp Ala Trp Leu Val Val Leu Leu Ala  
 675 680 685

Met Leu Val Glu Val Ala Leu Cys Thr Trp Tyr Leu Val Ala Phe Pro  
 690 695 700  
 Pro Glu Val Val Thr Asp Trp His Met Leu Pro Thr Glu Ala Leu Val  
 705 710 715 720  
 His Cys Arg Thr Arg Ser Trp Val Ser Phe Gly Leu Ala His Ala Thr  
 725 730 735  
 Asn Ala Thr Leu Ala Phe Leu Cys Phe Leu Gly Thr Phe Leu Val Arg  
 740 745 750  
 Ser Gln Pro Gly Cys Tyr Asn Arg Ala Arg Gly Leu Thr Phe Ala Met  
 755 760 765  
 Leu Ala Tyr Phe Ile Thr Trp Val Ser Phe Val Pro Leu Leu Ala Asn  
 770 775 780  
 Val Gln Val Val Leu Arg Pro Ala Val Gln Met Gly Ala Leu Leu Leu  
 785 790 795 800  
 Cys Val Leu Gly Ile Leu Ala Ala Phe His Leu Pro Arg Cys Tyr Leu  
 805 810 815  
 Leu Met Arg Gln Pro Gly Leu Asn Thr Pro Glu Phe Phe Leu Gly Gly  
 820 825 830  
 Gly Pro Gly Asp Ala Gln Gly Gln Asn Asp Gly Asn Thr Gly Asn Gln  
 835 840 845  
 Gly Lys His Glu  
 850

<210> 5  
 <211> 23  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Primer

<220>  
 <221> modified\_base  
 <222> (3)  
 <223> a, t, c, g, other or unknown

<220>  
 <221> modified\_base  
 <222> (9)  
 <223> a, t, c, g, other or unknown

<220>  
 <221> modified\_base  
 <222> (12)  
 <223> a, t, c, g, other or unknown



<220>  
 <221> modified\_base  
 <222> (18)  
 <223> a, t, c, g, other or unknown

<400> 5  
 cgnttyytng cntggggnga rcc

23

<210> 6  
 <211> 23  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Primer

<220>  
 <221> modified\_base  
 <222> (3)  
 <223> a, t, c, g, other or unknown

<220>  
 <221> modified\_base  
 <222> (6)  
 <223> a, t, c, g, other or unknown

<220>  
 <221> modified\_base  
 <222> (18)  
 <223> a, t, c, g, other or unknown

<220>  
 <221> modified\_base  
 <222> (21)  
 <223> a, t, c, g, other or unknown

<400> 6  
 cgngcncgrt trtarcance ngg

23

<210> 7  
 <211> 9  
 <212> PRT  
 <213> Homo sapiens

<400> 7  
 Arg Phe Leu Ala Trp Gly Glu Pro Ala  
 1 5

<210> 8  
 <211> 8  
 <212> PRT  
 <213> Homo sapiens

&lt;400&gt; 8

Pro Gly Cys Tyr Asn Arg Ala Arg

1

5

&lt;210&gt; 9

&lt;211&gt; 552

&lt;212&gt; DNA

&lt;213&gt; Mus sp.

&lt;400&gt; 9

```

gtgctgtcac tcctcctgct gctttgcctg gtgctgggct tagcactggc tgctctgggg 60
ctctctgtcc accactggga cagccctctt gtccaggcct caggcggctc acagttctgc 120
tttgccctga tctgcctagg cctcttctgc ctcagtgtcc ttctgttccc aggacggcca 180
agctctgcca gctgccttgc acaacaacca atggctcacc tccctctcac aggctgcctg 240
agcacactct tcctgcaagc agctgagacc tttgtggagt ctgagctgcc actgagctgg 300
gcaaactggc tatgcagcta ccttcgggac tctggcctgc tagtggtact gttggccact 360
tttgtggagg cagcactatg tgcctgggat ttgaccgctt caccagaagt ggtgacagac 420
tggtcagtcg tgcccacaga ggtactggag cactgccacg tgcgttctct ggtcaacctg 480
ggcttggtgc acatcaccaa tgcaatggta gcttttctct gctttctggg cactttctctg 540
gtacaagacc ag                                     552

```

&lt;210&gt; 10

&lt;211&gt; 184

&lt;212&gt; PRT

&lt;213&gt; Mus sp.

&lt;400&gt; 10

```

Val Leu Ser Leu Leu Leu Leu Cys Leu Val Leu Gly Leu Ala Leu
  1                      5                      10                      15

Ala Ala Leu Gly Leu Ser Val His His Trp Asp Ser Pro Leu Val Gln
      20                      25                      30

Ala Ser Gly Gly Ser Gln Phe Cys Phe Gly Leu Ile Cys Leu Gly Leu
      35                      40                      45

Phe Cys Leu Ser Val Leu Leu Phe Pro Gly Arg Pro Ser Ser Ala Ser
      50                      55                      60

Cys Leu Ala Gln Gln Pro Met Ala His Leu Pro Leu Thr Gly Cys Leu
      65                      70                      75                      80

Ser Thr Leu Phe Leu Gln Ala Ala Glu Thr Phe Val Glu Ser Glu Leu
      85                      90                      95

Pro Leu Ser Trp Ala Asn Trp Leu Cys Ser Tyr Leu Arg Asp Ser Gly
      100                     105                     110

Leu Leu Val Val Leu Leu Ala Thr Phe Val Glu Ala Ala Leu Cys Ala
      115                     120                     125

Trp Tyr Leu Thr Ala Ser Pro Glu Val Val Thr Asp Trp Ser Val Leu
      130                     135                     140

Pro Thr Glu Val Leu Glu His Cys His Val Arg Ser Trp Val Asn Leu
      145                     150                     155                     160

```

Gly Leu Val His Ile Thr Asn Ala Met Val Ala Phe Leu Cys Phe Leu  
 165 170 175

Gly Thr Phe Leu Val Gln Asp Gln  
 180

<210> 11  
 <211> 558  
 <212> DNA  
 <213> Rattus sp.

<400> 11  
 gtgctgtcac ttctcctgct gctttgcctg gtgctgggccc tgacactggc tgccttgggg 60  
 ctctttgtcc actactggga cagccctctt gttcaggcct cagggtgggtc actgttctgc 120  
 tttggcctga tctgcctagg cctcttctgc ctacagtgtcc ttctgttccc aggacgacca 180  
 cgctctgcca gctgccttgc ccaacaacca atggctcacc tccctctcac aggctgcctg 240  
 agcacactct tcttgaagc agccgagatc tttgtggagt ctgagctgcc actgagttgg 300  
 gcaaactggc tctgcagcta ccttcggggc ccctgggctt ggctgggtgg actgctggcc 360  
 actcttgggg aggtgcact atgtgcctgg tacttgatgg ctttccctcc agaggtgggtg 420  
 acagattggc aggtgctgcc cacggaggtg ctggaacact gccgcatgcg ttcctgggtc 480  
 agcctgggct tgggtgcacat caccaatgca ggggtagctt tcctctgctt tctgggcact 540  
 ttctggttac aaagccag 558

<210> 12  
 <211> 186  
 <212> PRT  
 <213> Rattus sp.

<400> 12  
 Val Leu Ser Leu Leu Leu Leu Cys Leu Val Leu Gly Leu Thr Leu  
 1 5 10 15  
 Ala Ala Leu Gly Leu Phe Val His Tyr Trp Asp Ser Pro Leu Val Gln  
 20 25 30  
 Ala Ser Gly Gly Ser Leu Phe Cys Phe Gly Leu Ile Cys Leu Gly Leu  
 35 40 45  
 Phe Cys Leu Ser Val Leu Leu Phe Pro Gly Arg Pro Arg Ser Ala Ser  
 50 55 60  
 Cys Leu Ala Gln Gln Pro Met Ala His Leu Pro Leu Thr Gly Cys Leu  
 65 70 75 80  
 Ser Thr Leu Phe Leu Gln Ala Ala Glu Ile Phe Val Glu Ser Glu Leu  
 85 90 95  
 Pro Leu Ser Trp Ala Asn Trp Leu Cys Ser Tyr Leu Arg Gly Pro Trp  
 100 105 110  
 Ala Trp Leu Val Val Leu Leu Ala Thr Leu Val Glu Ala Ala Leu Cys  
 115 120 125  
 Ala Trp Tyr Leu Met Ala Phe Pro Pro Glu Val Val Thr Asp Trp Gln  
 130 135 140

Val Leu Pro Thr Glu Val Leu Glu His Cys Arg Met Arg Ser Trp Val  
 145 150 155 160

Ser Leu Gly Leu Val His Ile Thr Asn Ala Gly Val Ala Phe Leu Cys  
 165 170 175

Phe Leu Gly Thr Phe Leu Val Gln Ser Gln  
 180 185

<210> 13

<211> 2577

<212> DNA

<213> Rattus sp.

<400> 13

atgccggggtt	tggtctatctt	gggcctcagt	ctggctgctt	tcctggagct	tgggatgggg	60
tcctctttgt	gtctgtcaca	gcaattcaag	gcacaagggg	actatatatt	gggtggacta	120
tttcccctgg	gcacaactga	ggaggccact	ctcaaccaga	gaacacagcc	caacggcatc	180
ctatgtacca	ggttctcgcc	ccttggtttg	ttcctggcca	tggtatgaa	gatggctgta	240
gaggagatca	acaatggatc	tgcttgctc	cctgggctgc	gactgggcta	tgacctgttt	300
gacacatgct	cagagccagt	ggtcaccatg	aagcccagcc	tcattgttcat	ggccaagggtg	360
ggaagtcaaa	gcattgctgc	ctactgcaac	tacacacagt	accaaccccc	tgtgctggct	420
gtcattgggtc	cccactcatc	agagcttgcc	ctcattacag	gcaagttctt	cagcttcttc	480
ctcatgccac	aggctcagcta	tagtgccagc	atggatcggc	taagtgaccg	ggaaacattt	540
ccatccttct	tccgcacagt	gcccagtgac	cgggtgcagc	tgaggccgt	tgtgacactg	600
ttgcagaatt	tcagctggaa	ctgggtgggt	gccttaggta	gtgatgatga	ctatggccgg	660
gaagggtctga	gcattcttttc	tggtctggcc	aactcacgag	gtatctgcat	tgcacacgag	720
ggcctgggtgc	cacaacatga	cactagtggc	caacaattgg	gcaaggtggg	ggatgtgcta	780
cgccaagtga	accaaagcaa	agtacagggt	gtgggtgctgt	ttgcatctgc	ccgtgctgtc	840
tactcccttt	ttagctacag	catccttcat	gacctctcac	ccaaggtatg	ggtggccagt	900
gagtcctggc	tgacctctga	cctggctcatg	acaactccca	atattgcccc	tgtgggcact	960
gttcttgggt	ttctgcagcg	cgggtgcccta	ctgcctgaat	tttccatta	tgtggagact	1020
cgcttggccc	tagctgctga	cccaacattc	tgtgcctccc	tgaaagctga	gttggatctg	1080
gaggagcgcg	tgatggggcc	acgctgttca	caatgtgact	acatcatgct	acagaacctg	1140
tcattctgggc	tgatgcagaa	cctatcagct	gggcagttgc	accaccaaatt	atttgcaacc	1200
tatgcagctg	tgtacagtgt	ggctcaggcc	cttcacaaca	ccctgcagtg	caatgtctca	1260
cattgccaca	catcagagcc	tggtcaacct	tggcagctcc	tggagaacat	gtacaatatg	1320
agtttccgtg	ctcgagactt	gacactgcag	tttgatgcc	aagggagtgt	agacatggaa	1380
tatgacctga	agatgtgggt	gtggcagagc	cctacacctg	tactacatac	tgtaggcacc	1440
ttcaacggca	cccttcagct	gcagcactcg	aaaatgtatt	ggccaggcaa	ccaggtgcca	1500
gtctcccagt	gctcccggca	gtgcaaagat	ggccaggtgc	gcagagtaaa	gggctttcat	1560
tcctgctgct	atgactgtgt	ggactgcaag	gcagggagct	accggaagca	tccagatgac	1620
ttcacctgta	ctccatgtgg	caaggatcag	tggtccccag	aaaaaagcac	aacctgctta	1680
cctcgcaggg	ccaagtttct	ggcttggggg	gagccagctg	tgctgtcact	tctcctgctg	1740
ctttgcctgg	tgctgggcct	gacactggct	gccctggggc	tctttgtcca	ctactgggac	1800
agccctcttg	ttcaggcctc	aggtgggtca	ctgttctgct	ttggcctgat	ctgcctaggc	1860
ctcttctgce	tcagtgtcct	tctgttccca	ggacgaccac	gctctgccag	ctgccttgcc	1920
caacaaccaa	tggtcacct	ccctctcaca	ggctgcctga	gcacactctt	cctgcaagca	1980
gccgagatct	ttgtggagtc	tgagctgcca	ctgagttggg	caaactggct	ctgcagctac	2040
cttcggggcc	cctgggcttg	gctggtggta	ctgctggcca	ctcttgtgga	ggctgacta	2100
tgtgcctggt	acttgatggc	tttccctcca	gaggtgggtga	cagattggca	ggtgctgccc	2160
acggaggtac	tggaaacttg	ccgcatgcgt	tcctgggtca	gcctgggctt	ggtgcacatc	2220
accaatgcag	tgttagcttt	cctctgcttt	ctgggcactt	tcctggtaca	gagccagcct	2280
ggtcgctata	accgtgcccg	tggcctcacc	ttcgccatgc	tagcttattt	catcatctgg	2340
gtctcttttg	tgcctctcct	ggctaattgtg	caggtggcct	accagccagc	tgtgcagatg	2400
ggtgctatct	tattctgtgc	cctgggcatc	ctggccacct	tccacctgcc	caaatgctat	2460

gtacttctgt ggctgccaga gctcaacacc caggagttct tcctgggaag gagccccaag 2520  
 gaagcatcag atgggaatag tggtagtagt gaggcaactc ggggacacag tgaatga 2577

<210> 14  
 <211> 858  
 <212> PRT  
 <213> Rattus sp.

<400> 14

Met	Pro	Gly	Leu	Ala	Ile	Leu	Gly	Leu	Ser	Leu	Ala	Ala	Phe	Leu	Glu
1				5					10					15	
Leu	Gly	Met	Gly	Ser	Ser	Leu	Cys	Leu	Ser	Gln	Gln	Phe	Lys	Ala	Gln
			20					25					30		
Gly	Asp	Tyr	Ile	Leu	Gly	Gly	Leu	Phe	Pro	Leu	Gly	Thr	Thr	Glu	Glu
		35					40					45			
Ala	Thr	Leu	Asn	Gln	Arg	Thr	Gln	Pro	Asn	Gly	Ile	Leu	Cys	Thr	Arg
	50					55					60				
Phe	Ser	Pro	Leu	Gly	Leu	Phe	Leu	Ala	Met	Ala	Met	Lys	Met	Ala	Val
65					70					75					80
Glu	Glu	Ile	Asn	Asn	Gly	Ser	Ala	Leu	Leu	Pro	Gly	Leu	Arg	Leu	Gly
				85					90					95	
Tyr	Asp	Leu	Phe	Asp	Thr	Cys	Ser	Glu	Pro	Val	Val	Thr	Met	Lys	Pro
		100						105					110		
Ser	Leu	Met	Phe	Met	Ala	Lys	Val	Gly	Ser	Gln	Ser	Ile	Ala	Ala	Tyr
		115					120					125			
Cys	Asn	Tyr	Thr	Gln	Tyr	Gln	Pro	Arg	Val	Leu	Ala	Val	Ile	Gly	Pro
	130					135					140				
His	Ser	Ser	Glu	Leu	Ala	Leu	Ile	Thr	Gly	Lys	Phe	Phe	Ser	Phe	Phe
145					150					155					160
Leu	Met	Pro	Gln	Val	Ser	Tyr	Ser	Ala	Ser	Met	Asp	Arg	Leu	Ser	Asp
				165					170					175	
Arg	Glu	Thr	Phe	Pro	Ser	Phe	Phe	Arg	Thr	Val	Pro	Ser	Asp	Arg	Val
			180					185					190		
Gln	Leu	Gln	Ala	Val	Val	Thr	Leu	Leu	Gln	Asn	Phe	Ser	Trp	Asn	Trp
	195						200					205			
Val	Ala	Ala	Leu	Gly	Ser	Asp	Asp	Asp	Tyr	Gly	Arg	Glu	Gly	Leu	Ser
	210					215					220				
Ile	Phe	Ser	Gly	Leu	Ala	Asn	Ser	Arg	Gly	Ile	Cys	Ile	Ala	His	Glu
225					230					235					240
Gly	Leu	Val	Pro	Gln	His	Asp	Thr	Ser	Gly	Gln	Gln	Leu	Gly	Lys	Val
				245					250					255	

Val	Asp	Val	Leu	Arg	Gln	Val	Asn	Gln	Ser	Lys	Val	Gln	Val	Val	Val	260	265	270	
Leu	Phe	Ala	Ser	Ala	Arg	Ala	Val	Tyr	Ser	Leu	Phe	Ser	Tyr	Ser	Ile	275	280	285	
Leu	His	Asp	Leu	Ser	Pro	Lys	Val	Trp	Val	Ala	Ser	Glu	Ser	Trp	Leu	290	295	300	
Thr	Ser	Asp	Leu	Val	Met	Thr	Leu	Pro	Asn	Ile	Ala	Arg	Val	Gly	Thr	305	310	315	320
Val	Leu	Gly	Phe	Leu	Gln	Arg	Gly	Ala	Leu	Leu	Pro	Glu	Phe	Ser	His	325	330	335	
Tyr	Val	Glu	Thr	Arg	Leu	Ala	Leu	Ala	Ala	Asp	Pro	Thr	Phe	Cys	Ala	340	345	350	
Ser	Leu	Lys	Ala	Glu	Leu	Asp	Leu	Glu	Glu	Arg	Val	Met	Gly	Pro	Arg	355	360	365	
Cys	Ser	Gln	Cys	Asp	Tyr	Ile	Met	Leu	Gln	Asn	Leu	Ser	Ser	Gly	Leu	370	375	380	
Met	Gln	Asn	Leu	Ser	Ala	Gly	Gln	Leu	His	His	Gln	Ile	Phe	Ala	Thr	385	390	395	400
Tyr	Ala	Ala	Val	Tyr	Ser	Val	Ala	Gln	Ala	Leu	His	Asn	Thr	Leu	Gln	405	410	415	
Cys	Asn	Val	Ser	His	Cys	His	Thr	Ser	Glu	Pro	Val	Gln	Pro	Trp	Gln	420	425	430	
Leu	Leu	Glu	Asn	Met	Tyr	Asn	Met	Ser	Phe	Arg	Ala	Arg	Asp	Leu	Thr	435	440	445	
Leu	Gln	Phe	Asp	Ala	Lys	Gly	Ser	Val	Asp	Met	Glu	Tyr	Asp	Leu	Lys	450	455	460	
Met	Trp	Val	Trp	Gln	Ser	Pro	Thr	Pro	Val	Leu	His	Thr	Val	Gly	Thr	465	470	475	480
Phe	Asn	Gly	Thr	Leu	Gln	Leu	Gln	His	Ser	Lys	Met	Tyr	Trp	Pro	Gly	485	490	495	
Asn	Gln	Val	Pro	Val	Ser	Gln	Cys	Ser	Arg	Gln	Cys	Lys	Asp	Gly	Gln	500	505	510	
Val	Arg	Arg	Val	Lys	Gly	Phe	His	Ser	Cys	Cys	Tyr	Asp	Cys	Val	Asp	515	520	525	
Cys	Lys	Ala	Gly	Ser	Tyr	Arg	Lys	His	Pro	Asp	Asp	Phe	Thr	Cys	Thr	530	535	540	
Pro	Cys	Gly	Lys	Asp	Gln	Trp	Ser	Pro	Glu	Lys	Ser	Thr	Thr	Cys	Leu	545	550	555	560

Pro Arg Arg Pro Lys Phe Leu Ala Trp Gly Glu Pro Ala Val Leu Ser  
 565 570 575  
 Leu Leu Leu Leu Leu Cys Leu Val Leu Gly Leu Thr Leu Ala Ala Leu  
 580 585 590  
 Gly Leu Phe Val His Tyr Trp Asp Ser Pro Leu Val Gln Ala Ser Gly  
 595 600 605  
 Gly Ser Leu Phe Cys Phe Gly Leu Ile Cys Leu Gly Leu Phe Cys Leu  
 610 615 620  
 Ser Val Leu Leu Phe Pro Gly Arg Pro Arg Ser Ala Ser Cys Leu Ala  
 625 630 635 640  
 Gln Gln Pro Met Ala His Leu Pro Leu Thr Gly Cys Leu Ser Thr Leu  
 645 650 655  
 Phe Leu Gln Ala Ala Glu Ile Phe Val Glu Ser Glu Leu Pro Leu Ser  
 660 665 670  
 Trp Ala Asn Trp Leu Cys Ser Tyr Leu Arg Gly Pro Trp Ala Trp Leu  
 675 680 685  
 Val Val Leu Leu Ala Thr Leu Val Glu Ala Ala Leu Cys Ala Trp Tyr  
 690 700  
 Leu Met Ala Phe Pro Pro Glu Val Val Thr Asp Trp Gln Val Leu Pro  
 705 710 715 720  
 Thr Glu Val Leu Glu His Cys Arg Met Arg Ser Trp Val Ser Leu Gly  
 725 730 735  
 Leu Val His Ile Thr Asn Ala Val Leu Ala Phe Leu Cys Phe Leu Gly  
 740 745 750  
 Thr Phe Leu Val Gln Ser Gln Pro Gly Arg Tyr Asn Arg Ala Arg Gly  
 755 760 765  
 Leu Thr Phe Ala Met Leu Ala Tyr Phe Ile Ile Trp Val Ser Phe Val  
 770 775 780  
 Pro Leu Leu Ala Asn Val Gln Val Ala Tyr Gln Pro Ala Val Gln Met  
 785 790 795 800  
 Gly Ala Ile Leu Phe Cys Ala Leu Gly Ile Leu Ala Thr Phe His Leu  
 805 810 815  
 Pro Lys Cys Tyr Val Leu Leu Trp Leu Pro Glu Leu Asn Thr Gln Glu  
 820 825 830  
 Phe Phe Leu Gly Arg Ser Pro Lys Glu Ala Ser Asp Gly Asn Ser Gly  
 835 840 845  
 Ser Ser Glu Ala Thr Arg Gly His Ser Glu  
 850 855

<210> 15  
 <211> 8194  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> modified\_base  
 <222> (1251)..(1300)  
 <223> a, t, c, g, other or unknown

<220>  
 <221> modified\_base  
 <222> (1951)..(2000)  
 <223> a, t, c, g, other or unknown

<400> 15  
 gagaatctcg cgagatcccg tcggtccgcc ccgctgccct cccagctgcc gaaaagaggg 60  
 gcctccgagc cgccggcgcc ctctgccggc aacctccgga agcacactag gaggttccag 120  
 ccgatctggt cgaggggctc cacggaggac tccatttacg ttacgcaa atccctacccc 180  
 agccggccgg agagagaaaag ccagaaacct cgcgaccagc catggggcac ctctccggaa 240  
 aaacaccggg atattttttt tctcctgcag aaaaagcttt aggattggca gtttaaacia 300  
 aacatgtcta tttgcatacc ttcggtttgc atgcatttgt ttcgaagtga gcaaccttgg 360  
 gtaacaaggc gaaagtatat gacaatttgc tcagaatctt aatgtcagaa aactggagac 420  
 tggggcaggg ggggtgtcgac tcaaagctgt gtctcattta gtaaactgag gccaggttaa 480  
 aaagtcttga aacctcgcaa caccgggaga aatttgtgtc cagcctccca cctcgcccca 540  
 aaatgccaga gctccttttc taagccaggc gaagtcacag agcgtggaca gaaccacaaa 600  
 ccgtccagag gaagggtcac tgggtgccac ctggtttgca tctgtgcctt cgtcctgccc 660  
 agttcctgag tgggaccgca ggcccggaat gtcaaaggca acagtcctgc ttcagccact 720  
 gggctccagt cccacccctt ttgggggccc gaagttagga agcatccggc agctgccttc 780  
 tatttaagca actggcctcc ttagaggcca ctcttgccc atgccaggcg cgggcatctg 840  
 gccagcatgc tgcctcgcac ggctcgcctg gtccggcctg agcttctcat ttcctgctgc 900  
 tgggcctttg cctgccatag cacggagtct tctcctgact tcacctccc cggagattac 960  
 ctcttgccag gcctgttccc tctccattct ggctgtctgc aggtgaggca cagaccgag 1020  
 gtgaccctgt gtgacaggtg agtgaggggc cagcagagcc acacttagtg ggacccttg 1080  
 ctatagggcc cctctggctg ccctcctcca aacaggacct tgcctctgccc tttgcccctt 1140  
 gaactgtccc caggccttgt tcatcaatcc acttgccacc taagtgtctg ctagaccttc 1200  
 ctagacactt cggccagttt ccaattattt cacccttgct gttagaatgt nnnnnnnnnn 1260  
 nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn aattccttaa actaaatttc 1320  
 tcactttctc tctctctctg gaaaacactg actaatgtag caggtttctc tgctccagga 1380  
 cttcaggacc ttttcgatgc taataagttt ctccatcagg gccagcttgt tctcctact 1440  
 gagcttgaga gcccttggtg aagttgtggt ttgggggact ggaccgatga cctcaaaggt 1500  
 tccctttgct cccaagctc agagtctagg aggccagagg gtctcagcag gcctttgtcc 1560  
 ttctcagctg tctcttactg gctttctcca caggtcttgt agcttcaatg agcatggcta 1620  
 ccacctcttc caggctatgc ggcttggggg tgaggagata aacaactcca cggccctgct 1680  
 gcccaacatc accctggggg accagctgta tgatgtgtgt tctgactctg ccaatgtgta 1740  
 tgccacgctg agagtgtctt ccctgccagg gcaacaccac atagagctcc aaggagacct 1800  
 tctccactat tcccctacgg tgcctggcag gattgggccc gacagcacca accgtgctgc 1860  
 caccacagcc gccctgctga gccctttcct ggtgcccctg gtaagctgga gcctcagacc 1920  
 tttgcccctc tcccctcagg caagtctggg nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn 1980  
 nnnnnnnnnn nnnnnnnnnn gccaccatgc ccggctaatt tttttgtatt tttagtagag 2040  
 acgggggttc accgtgttag ccaggctggt cgcaaactcc taacctctgt atccaccac 2100  
 ctgggctccc caatgtgctg ggattacagg tgtgagccac tgcaccggc cataatgtat 2160  
 taatataata aaataattat acaactcacc ataatgtaga atcagtggga gcctgagct 2220  
 tgttttccta caactagatg gtcccatctg ggggtgatgg gagacagtga cagatcatca 2280  
 gacattagat tctcataagt agcgtgcaac ccagatccct cgcagtgtga gttcacagta 2340  
 gggttcaagc tccataaaga atctgatgct cgtgctgac tgacaggagg ggagcagctg 2400  
 taaatacaga tgaagcttcg cttactcacc agctgctcac ctcctcctgt gagggccggg 2460  
 tcctaacagg ccactgacct aacttctgcc ctgacctaca catgcttctc ttcttccttg 2520



caaactgcct	ccagtgggaag	tccctgaagg	tccccaacaa	cacgggacta	tttcaactcct	2580
atgcaggttt	tgtctccttt	gcttggaatg	catccccca	ccccttgtcc	ccaggcagat	2640
tcccaccct	cccccagaac	ctgccccagt	ggagccttcg	caggtgattt	gtcagtttca	2700
caggctgagg	ggtgctctcc	tggctcctcc	ggctccctgt	atccccacac	ccagcacagg	2760
gccaggcact	gggggggcct	tcaagtggaga	ctgaaatggc	tgaacgggac	ctcccataga	2820
ttagctatgc	ggccagcagc	gagacgctca	gcgtgaagcg	gcagtatccc	tctttcctgc	2880
gcaccatccc	caatgacaag	taccagggtg	agaccatggg	gctgctgctg	cagaagttcg	2940
ggtggacctg	gatctctctg	gttggcagca	gtgacgacta	tgggcagcta	ggggtgcagg	3000
cactggagaa	ccaggccact	ggtcagggga	tctgcattgc	tttcaaggac	atcatgccct	3060
tctctgcca	ggtgggcgat	gagaggatgc	agtgcctcat	gcgccacctg	gcccaggccg	3120
gggccaccgt	cgtggttggt	ttttccagcc	ggcagttggc	caggggtgtt	ttcgagtccg	3180
tgggtgctgac	caacctgact	ggcaagggtg	gggtgcctc	agaagcctgg	gccctctcca	3240
ggcacatcac	tggggtgccc	gggatccagc	gcattgggat	ggtgctgggc	gtggccatcc	3300
agaagaggcg	tgccccggc	ctgaaggcgt	ttgaagaagc	ctatgcccg	gcagacaaga	3360
aggccccctag	gccttgccac	aagggtcctc	ggtgcagcag	caatcagctc	tcagagaaat	3420
gccaagcttt	catggcacac	acgatgcccc	agctcaaagc	cttctccatg	agttctgcct	3480
acaacgcata	cggggtctgt	tatgcggtgg	cccatggcct	ccaccagctc	ctgggctgtg	3540
cctctggagc	ttgttccagg	ggccgagtct	acccctggca	ggtaagagag	cccacccccag	3600
cacctcctgt	caggggagaac	agccaatcct	gagatgagca	gagtgggcac	tctccgggtca	3660
ctctaaatgc	caagggggat	aaatgccact	aaattgaggt	tttttgtttt	gttttgtttt	3720
gttttttag	acagctggc	tctgtcacc	aggctgcagt	gtagtgatgc	gatctcggct	3780
ctctgcaact	tccacctcct	gggttcaagt	gattctcttg	cctcggcctc	ctgagtagct	3840
gggattacag	gcacccacca	ccatgcctgg	ataatttttc	ttttcttttt	tttttttttg	3900
agatagagtc	tcgctctgtt	gcccaggctg	gaatgcagtg	gtgcgatctt	ggctcactgt	3960
gagctccgcc	tcccaggttc	actccattcc	cctgcctcag	cctcccaagt	aggtgggact	4020
acggggcggc	gccaccacgc	ccagctaatt	ttttttgtat	tttgagtaga	gacgggggtt	4080
caccatgtta	gccaggatgg	tctcaatctc	ctgacctgtg	catccgcccc	cctcgtcctc	4140
ccaaagtgtc	gggattacag	gcgtgagcca	cgcgaccgg	cctaattttt	gtatttttag	4200
tagagatggg	gtttcaccat	gttggccagg	ctgggtctga	actcctggca	tcaagtgatc	4260
ctcctgcttc	ggcctcccaa	agtgtcggga	ttacaggcat	tagctctctt	ctcttagaca	4320
gatctttctc	tctgatcctt	gccttctctc	acccactgtg	tcttggaagt	gtcaagtgat	4380
aagatccagg	gctaaaactg	tctgtaaaag	agtgtttgtt	agaggcctcc	tctcaggagg	4440
ttggtgggga	agattgaggg	gcttcctaag	aagggaaggga	cgagaccttc	ctgatgggct	4500
gaaaccacca	ggacggaaac	ccaggaaggc	cccaggccct	tgcttctggg	accatgtggg	4560
tctgtgctgt	ctgtgggtgg	ttcatgatac	gcgtttcttt	cagcttttgg	agcagatcca	4620
caaggtgcat	ttccttctac	acaaggacac	tgtggcggtt	aatgacaaca	gagatccctt	4680
cagtagctat	aacataattg	cctgggactg	gaatggaccc	aagtggacct	tcacggctct	4740
cggttcctcc	acatggtctc	cagttcagct	aaacataaat	gagaccaaaa	tccagtggca	4800
cggaaaggac	aaccaggtaa	tggggatgtg	gctactcacc	atgtaactgg	cttatgggca	4860
acctagagcc	tgggggtgat	gctgacacag	tgtacaggga	gcaggagggg	ggccccaggg	4920
gtccagctgc	caccactcta	cccatcctgg	ccaggggaagc	agggaagaca	ctccgtaggc	4980
gagtggtcag	atgccctggg	gcggaagttc	acacgaccag	gggcccctgc	ctgggagtgga	5040
gccctgaggg	cagatgcaca	gagattctgt	tttctgttcc	acatgtgagc	tgtcctttga	5100
cttgggcccc	tacgtgtggc	ccctctggct	tcttacagg	gcctaagtct	gtgtgttcca	5160
gcgactgtct	tgaagggcac	cagcgagtgg	ttacgggttt	ccatcactgc	tgctttgagt	5220
gtgtgccttg	tggggctggg	accttcctca	acaagagtgg	tgagtgggca	atggagcagg	5280
cgagctaccc	agcactccc	ggggctgcac	ggtggaggga	gggcctcctt	tgggccccat	5340
gtgccctgcc	ccagaaccaa	ggcccagtca	ctgggctgcc	agttagcttc	aggttgagg	5400
acacctgcta	ccagacagaa	ttctgatcaa	gagaatcagc	cactgggtgc	ggtggctcat	5460
gcctgtaatc	ccagcacttt	gggaggctga	ggcgggtgga	tcacttgagg	tcgggagttc	5520
gagaccagcc	tggccaacat	ggtgaaaccc	catctctacc	aaaaatataa	aaaattagct	5580
gggtgtggtg	gcgcgtgcct	gtaatcccag	ctactcggga	ggctgaggca	ggagaatcac	5640
ttgaacccag	gaggcgagg	ttgcagtgag	ccaagatgca	ttccagcctg	gaccacaaag	5700
cgagaattcg	tcccccaaa	aaaagaaagg	aggccgggcg	cggtggctca	cacctgtaat	5760
cccagcactt	tgggagggcg	agggtgggtg	atcacctgag	gtcaggagtt	cgagaccagc	5820
ctgaccaaca	ttgggtgaaacc	ccatctctac	taaaaaataca	aaaaaagtta	gccgggctgt	5880
gtggcggtgtg	cctgtaattc	cagctactcg	ggaggctgag	gcaggagaat	tgcttgaacc	5940
cgggaggcgg	aggttgacgt	gagccaagat	tgcaccattg	cactccagcc	tgggcgacaa	6000

gagaaaaact	ctgtctcaaa	aaaaaagaaa	gaaagaaaga	attagccaac	tgaaagcctt	6060
agactgaggt	gtgtcctctg	ttagagagct	gtcatcacaa	ctcctacaaa	agcagtcgta	6120
tcctgaattc	aacctctttc	tctaaatgaa	tatagctatt	gttccctttg	tgccctcttg	6180
tcctactgtc	ccttctgttg	cccatgccaa	agacagctag	ctccttgaaac	agcttggcct	6240
gaatacagat	actagcgtgt	ctgcagcaga	gaaaaaaaca	gcattcccca	tccagaaatg	6300
caaggtcaag	aacagagagc	aaattaggtg	gctaaggact	caggtectta	gttgggtgcc	6360
aggggccaca	ttcttttcct	tcacatcttc	tgtagggaca	ggaatacttc	ccttctgtcc	6420
tcagaggggtc	aggactcaga	gaaaccacag	agcagcagct	caggaaagtg	gttcatggaa	6480
atgctggcaa	gagagagggg	ttacaatgcc	ctcccttggg	agcaggctgc	ttccatcaga	6540
tcgtaacctc	tctgggtatg	gggcagagct	accaggttaa	ggctcctcct	agggtttgca	6600
aaacctcat	gggatcatga	gccatacaga	accgacctgt	gtgtctccag	agtctgtaat	6660
taacacaggc	atttttgagga	aatgcgtggc	ctcaggcccc	actcccggtc	acccccatcc	6720
cactatgcct	agtatagctc	agctgccttg	gtacaattct	cccagtatct	tgaggcccc	6780
tatttcctat	tctactctgt	ctcatctggc	ctcagggaac	cttcttggcc	ttccctttca	6840
gacctctaca	gatgccagcc	ttgtgggaaa	gaagagtggg	cacctgaggg	aagccagacc	6900
tgcttcccgc	gcactgtggt	gttttttggt	ttgcgtgagc	acacctcttg	ggtgctgctg	6960
gcagctaaca	cgctgctgct	gctgctgctg	cttgggactg	ctggcctgtt	tgctggcac	7020
ctagacaccc	ctgtggtgag	gtcagcaggg	ggcgcctgt	gctttcttat	gctgggctcc	7080
ctggcagcag	gtagtggcag	cctctatggc	ttctttgggg	aaccacaaag	gcctgcgtgc	7140
ttgctacgcc	aggccctctt	tgcccttggt	ttcaccatct	tcctgtcctg	cctgacagtt	7200
cgctacatcc	aactaatcat	catcttcaag	ttttccacca	aggtacctac	attctaccac	7260
gcctgggtcc	aaaaccacgg	tgctggcctg	tttgtgatga	tcagctcagc	ggcccagctg	7320
cttatctgtc	taacttggct	ggtgggtgtg	acccactgc	ctgctaggga	ataccagcgc	7380
ttcccccatc	tgggtgatgt	tgagtgcaca	gagaccaact	ccctgggctt	catactggcc	7440
ttcctctaca	atggcctcct	ctccatcagt	gcctttgcct	gcagctacct	gggtaaggac	7500
ttgccagaga	actacaacga	ggccaaatgt	gtcaccttca	gcctgctctt	caacttcgtg	7560
tcttgatcg	ccttcttcac	cacggccagc	gtctacgacg	gcaagtacct	gcctgcggcc	7620
aacatgatgg	ctgggctgag	cagcctgagc	agcggcttcg	gtgggtatatt	tctgcctaag	7680
tgctacgtga	tcctctgcgg	cccagacctc	aacagcacag	agcaactcca	ggcctccatt	7740
caggactaca	cgaggcgctg	cggctccacc	tgaccagtgg	gtcagcaggg	acggctggca	7800
gccttctctg	ccctgagggg	cgaaggctga	gcaggccggg	ggtgtccggg	aggctcttgg	7860
gcatcgcggt	ctgggggttg	gacgtgtaag	cgcttgggag	agcctagacc	aggctccggg	7920
ctgccataaa	agaagtgaag	tgcgatatctg	gtctcctgtc	gtgggagagt	gtgaggtgta	7980
acggattcaa	gtctgaacct	agagcctgga	aaaggctgac	cgcccagatt	gacgttgcta	8040
ggcaactccg	gaggcgggcc	cagcgccaaa	agaacagggc	gaggcgctcg	ccccgcatac	8100
cattggccgt	tctctgcggg	gccccgcctt	cgggggcccg	agctagaagc	tctacgcttc	8160
cgaggcgcac	ctcctggcct	gcacgctttg	acgt			8194

&lt;210&gt; 16

&lt;211&gt; 2526

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 16

atgctgctct	gcacggctcg	cctggctcggc	ctgcagcttc	tcatttctctg	ctgctggggc	60
tttgctgcc	atagcacgga	gtcttctcct	gacttcaccc	tccccggaga	ttacctctg	120
gcaggcctgt	tcctctcca	ttctggctgt	ctgcagggtga	ggcacagacc	cgaggtgacc	180
ctgtgtgaca	ggctctgtag	cttcaatgag	catggctacc	acctcttcca	ggctatgcgg	240
cttgggggtg	aggagataaa	caactccacg	gccctgctgc	ccaacatcac	cctgggggtac	300
cagctgtatg	atgtgtgttc	tgactctgcc	aatgtgtatg	ccacgctgag	agtgtctctc	360
ctgccagggc	aacaccacat	agagctccaa	ggagaccttc	tccactattc	ccctacggtg	420
ctggcagtg	ttgggcctga	cagcaccaac	cgtgctgcca	ccacagccgc	cctgctgagc	480
cctttcctgg	tgcccatgat	tagctatgcg	gccagcagcg	agacgctcag	cgtgaagcgg	540
cagtatccct	ctttcctgcg	caccatcccc	aatgacaagt	accaggtgga	gaccatggtg	600
ctgctgctgc	agaagtccg	gtggacctgg	atctctctgg	ttggcagcag	tgacgactat	660
gggcagctag	gggtgcaggc	actggagaac	caggccactg	gtcaggggat	ctgcattgct	720
ttcaaggaca	tcatgccctt	ctctgcccag	gtgggcgatg	agaggatgca	gtgcctcatg	780

```

cgccacctgg cccaggccgg ggccaccgtc gtggttggtt tttccagccg gcagttggcc 840
aggggtgttt tcgagtcctg ggtgctgacc aacctgactg gcaaggtgtg ggtcgctca 900
gaagcctggg ccctctccag gcacatcact ggggtgcccg ggatccagcg cattgggatg 960
gtgctgggcg tggccatcca gaagagggct gtccctggcc tgaaggcggt tgaagaagcc 1020
tatgcccggg cagacaagaa ggcccctagg ccttgccaca agggctcctg gtgcagcagc 1080
aatcagctct gcagagaatg ccaagctttc atggcacaca cgatgcccaa gctcaaagcc 1140
ttctccatga gttctgccta caacgcatac cgggctgtgt atgcggtggc ccatggcctc 1200
caccagctcc tgggctgtgc ctctggagct tgttccaggg gccgagtcta cccctggcag 1260
cttttgagc agatccacaa ggtgcatttc cttctacaca aggacactgt ggcgtttaat 1320
gacaacagag atccctcag tagctataac ataattgcct gggactggaa tggaccaag 1380
tggaacctca cggctcctcg ttcctccaca tggctccag ttcagctaaa cataaatgag 1440
acaaaaatcc agtggcacgg aaaggacaac caggtgccta agtctgtgtg ttccagcgac 1500
tgtcttgaag ggcaccagcg agtgggttac ggtttccatc actgctgctt tgagtgtgtg 1560
cccttggggg cgtggacctt cctcaacaag agtgacctct acagatgcca gccttggtggg 1620
aaagaagagt gggcacctga gggaagccag acctgcttcc cgcgcactgt ggtgtttttg 1680
gctttgcgtg agcacacctc ttgggtgctg ctggcagcta acacgctgct gctgctgctg 1740
ctgcttgagg ctgctggcct gtttgcttgg cacttagaca cccctgtggt gaggtcagca 1800
ggggggccgc tgtgctttct tatgctgggc tccttggcag caggtagtgg cagcctctat 1860
ggcttctttg gggaacccac aaggcctgcg tgcctgctac gccaggccct ctttgccctt 1920
ggtttcacca tcttctgtc ctgcctgaca gttcgctcat tccaaactat catcatcttc 1980
aagttttcca ccaaggtacc tacattctac cagcctggg tccaaaacca cgggtgctggc 2040
ctggttggtg tgatcagctc agcggcccg ctgcttatct gtctaacttg gctgggtgtg 2100
tggaacccac tgcctgctag ggaataccag cgcttcccc atctggtgat gcttgagtgc 2160
acagagacca actccttggg cttcatactg gccttctct acaatggcct cctctccatc 2220
agtgcctttg cctgcagcta cctgggtaag gacttgccag agaactacaa cgaggccaaa 2280
tgtgtcacct tcagcctgct cttcaacttc gtgtcctgga tcgccttctt caccacggcc 2340
agcgtctacg acggcaagta cctgcctgcg gccaacatga tggctgggct gagcagcctg 2400
agcagcggct tcggtgggta ttttctgcct aagtgtctac tgatcctctg ccgcccagac 2460
ctcaacagca cagagcactt ccaggcctcc attcaggact acacgaggcg ctgcggctcc 2520
acctga 2526

```

<210> 17

<211> 841

<212> PRT

<213> Homo sapiens

<400> 17

```

Met Leu Leu Cys Thr Ala Arg Leu Val Gly Leu Gln Leu Leu Ile Ser
 1              5              10              15

Cys Cys Trp Ala Phe Ala Cys His Ser Thr Glu Ser Ser Pro Asp Phe
      20              25              30

Thr Leu Pro Gly Asp Tyr Leu Leu Ala Gly Leu Phe Pro Leu His Ser
      35              40              45

Gly Cys Leu Gln Val Arg His Arg Pro Glu Val Thr Leu Cys Asp Arg
      50              55              60

Ser Cys Ser Phe Asn Glu His Gly Tyr His Leu Phe Gln Ala Met Arg
      65              70              75              80

Leu Gly Val Glu Glu Ile Asn Asn Ser Thr Ala Leu Leu Pro Asn Ile
      85              90              95

Thr Leu Gly Tyr Gln Leu Tyr Asp Val Cys Ser Asp Ser Ala Asn Val
      100              105              110

```

Tyr Ala Thr Leu Arg Val Leu Ser Leu Pro Gly Gln His His Ile Glu  
 115 120 125  
 Leu Gln Gly Asp Leu Leu His Tyr Ser Pro Thr Val Leu Ala Val Ile  
 130 135 140  
 Gly Pro Asp Ser Thr Asn Arg Ala Ala Thr Thr Ala Ala Leu Leu Ser  
 145 150 155 160  
 Pro Phe Leu Val Pro Met Ile Ser Tyr Ala Ala Ser Ser Glu Thr Leu  
 165 170 175  
 Ser Val Lys Arg Gln Tyr Pro Ser Phe Leu Arg Thr Ile Pro Asn Asp  
 180 185 190  
 Lys Tyr Gln Val Glu Thr Met Val Leu Leu Leu Gln Lys Phe Gly Trp  
 195 200 205  
 Thr Trp Ile Ser Leu Val Gly Ser Ser Asp Asp Tyr Gly Gln Leu Gly  
 210 215 220  
 Val Gln Ala Leu Glu Asn Gln Ala Thr Gly Gln Gly Ile Cys Ile Ala  
 225 230 235 240  
 Phe Lys Asp Ile Met Pro Phe Ser Ala Gln Val Gly Asp Glu Arg Met  
 245 250 255  
 Gln Cys Leu Met Arg His Leu Ala Gln Ala Gly Ala Thr Val Val Val  
 260 265 270  
 Val Phe Ser Ser Arg Gln Leu Ala Arg Val Phe Phe Glu Ser Val Val  
 275 280 285  
 Leu Thr Asn Leu Thr Gly Lys Val Trp Val Ala Ser Glu Ala Trp Ala  
 290 295 300  
 Leu Ser Arg His Ile Thr Gly Val Pro Gly Ile Gln Arg Ile Gly Met  
 305 310 315 320  
 Val Leu Gly Val Ala Ile Gln Lys Arg Ala Val Pro Gly Leu Lys Ala  
 325 330 335  
 Phe Glu Glu Ala Tyr Ala Arg Ala Asp Lys Lys Ala Pro Arg Pro Cys  
 340 345 350  
 His Lys Gly Ser Trp Cys Ser Ser Asn Gln Leu Cys Arg Glu Cys Gln  
 355 360 365  
 Ala Phe Met Ala His Thr Met Pro Lys Leu Lys Ala Phe Ser Met Ser  
 370 375 380  
 Ser Ala Tyr Asn Ala Tyr Arg Ala Val Tyr Ala Val Ala His Gly Leu  
 385 390 395 400  
 His Gln Leu Leu Gly Cys Ala Ser Gly Ala Cys Ser Arg Gly Arg Val  
 405 410 415

Tyr Pro Trp Gln Leu Leu Glu Gln Ile His Lys Val His Phe Leu Leu  
 420 425 430  
 His Lys Asp Thr Val Ala Phe Asn Asp Asn Arg Asp Pro Leu Ser Ser  
 435 440 445  
 Tyr Asn Ile Ile Ala Trp Asp Trp Asn Gly Pro Lys Trp Thr Phe Thr  
 450 455 460  
 Val Leu Gly Ser Ser Thr Trp Ser Pro Val Gln Leu Asn Ile Asn Glu  
 465 470 475 480  
 Thr Lys Ile Gln Trp His Gly Lys Asp Asn Gln Val Pro Lys Ser Val  
 485 490 495  
 Cys Ser Ser Asp Cys Leu Glu Gly His Gln Arg Val Val Thr Gly Phe  
 500 505 510  
 His His Cys Cys Phe Glu Cys Val Pro Cys Gly Ala Gly Thr Phe Leu  
 515 520 525  
 Asn Lys Ser Asp Leu Tyr Arg Cys Gln Pro Cys Gly Lys Glu Glu Trp  
 530 535 540  
 Ala Pro Glu Gly Ser Gln Thr Cys Phe Pro Arg Thr Val Val Phe Leu  
 545 550 555 560  
 Ala Leu Arg Glu His Thr Ser Trp Val Leu Leu Ala Ala Asn Thr Leu  
 565 570 575  
 Leu Leu Leu Leu Leu Leu Gly Thr Ala Gly Leu Phe Ala Trp His Leu  
 580 585 590  
 Asp Thr Pro Val Val Arg Ser Ala Gly Gly Arg Leu Cys Phe Leu Met  
 595 600 605  
 Leu Gly Ser Leu Ala Ala Gly Ser Gly Ser Leu Tyr Gly Phe Phe Gly  
 610 615 620  
 Glu Pro Thr Arg Pro Ala Cys Leu Leu Arg Gln Ala Leu Phe Ala Leu  
 625 630 635 640  
 Gly Phe Thr Ile Phe Leu Ser Cys Leu Thr Val Arg Ser Phe Gln Leu  
 645 650 655  
 Ile Ile Ile Phe Lys Phe Ser Thr Lys Val Pro Thr Phe Tyr His Ala  
 660 665 670  
 Trp Val Gln Asn His Gly Ala Gly Leu Phe Val Met Ile Ser Ser Ala  
 675 680 685  
 Ala Gln Leu Leu Ile Cys Leu Thr Trp Leu Val Val Trp Thr Pro Leu  
 690 695 700  
 Pro Ala Arg Glu Tyr Gln Arg Phe Pro His Leu Val Met Leu Glu Cys  
 705 710 715 720

Thr Glu Thr Asn Ser Leu Gly Phe Ile Leu Ala Phe Leu Tyr Asn Gly  
                               725                              730                              735  
 Leu Leu Ser Ile Ser Ala Phe Ala Cys Ser Tyr Leu Gly Lys Asp Leu  
                               740                              745                              750  
 Pro Glu Asn Tyr Asn Glu Ala Lys Cys Val Thr Phe Ser Leu Leu Phe  
                               755                              760                              765  
 Asn Phe Val Ser Trp Ile Ala Phe Phe Thr Thr Ala Ser Val Tyr Asp  
                               770                              775                              780  
 Gly Lys Tyr Leu Pro Ala Ala Asn Met Met Ala Gly Leu Ser Ser Leu  
                               785                              790                              795                              800  
 Ser Ser Gly Phe Gly Gly Tyr Phe Leu Pro Lys Cys Tyr Val Ile Leu  
                               805                              810                              815  
 Cys Arg Pro Asp Leu Asn Ser Thr Glu His Phe Gln Ala Ser Ile Gln  
                               820                              825                              830  
 Asp Tyr Thr Arg Arg Cys Gly Ser Thr  
                               835                              840

<210> 18

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Consensus  
sequence

<220>

<221> MOD\_RES

<222> (1)

<223> Thr or Arg

<220>

<221> MOD\_RES

<222> (3)

<223> Phe or Leu

<220>

<221> MOD\_RES

<222> (4)

<223> Arg, Gln or Pro

<220>

<221> MOD\_RES

<222> (6)

<223> Arg or Thr

<220>

<221> MOD\_RES

<222> (7)

<223> Ser, Pro or Val

<400> 18  
Xaa Cys Xaa Xaa Arg Xaa Xaa Xaa Phe Leu Xaa Xaa Xaa Glu  
1 5 10

```
<210> 19
<211> 15
<212> PRT
<213> Artificial Sequence
```

```
<220>
<223> Description of Artificial Sequence: Consensus
sequence
```

```
<220>  
<221> MOD_RES  
<222> (1)  
<223> Leu or Gln
```

```
<220>
<221> MOD_RES
<222> (3)
<223> Glu, Gly or Thr
```

```
<220>  
<221> MOD_RES  
<222> (4)  
<223> Asn, Arg or Cys
```

```
<220>
<221> MOD_RES
<222> (7)
<223> Arg or Glu
```

```
<220>  
<221> MOD_RES  
<222> (9)
```

<223> Arg or Lys

<220>

<221> MOD\_RES

<222> (10)

<223> Cys, Gly or Phe

<220>

<221> MOD\_RES

<222> (11)

<223> Val, Leu or Ile

<220>

<221> MOD\_RES

<222> (13)

<223> Phe or Leu

<220>

<221> MOD\_RES

<222> (14)

<223> Ala or Ser

<220>

<221> MOD\_RES

<222> (15)

<223> Met or Leu

<400> 19

Xaa Pro Xaa Xaa Tyr Asn Xaa Ala Xaa Xaa Xaa Thr Xaa Xaa Xaa

1

5

10

15

<210> 20

<211> 3563

<212> DNA

<213> Homo sapiens

<400> 20

```

agcctggcag tggcctcagg cagagtctga cgcgcacaaa ctttcaggcc caggaagcga 60
ggacaccact ggggccccag ggtgtggcaa gtgaggatgg caagggtttt gctaaacaaa 120
tcctctgccc gctccccgcc ccgggctcac tccatgtgag gccccagtcg gggcagccac 180
ctgccgtgcc tgttggaagt tgcctctgcc atgctgggcc ctgctgtcct gggcctcagc 240
ctctgggctc tcctgcaccc tgggacgggg gccccattgt gcctgtcaca gcaacttagg 300
atgaaggggg actacgtgct gggggggctg ttccccctgg gcgaggccga ggaggctggc 360
ctccgcagcc ggacacggcc cagcagccct gtgtgcacca ggtacagagg tgggacggcc 420
tgggtcgggg tcagggtgac caggtctggg gtgctcctga gctggggccg aggtggccat 480
ctgcggttct gtgtggcccc aggttctcct caaacggcct gctctgggca ctggccatga 540
aaatggccgt ggaggagatc aacaacaagt cggatctgct gcccgggctg cgcctgggct 600
acgacctctt tgatacgtgc tcggagcctg tgggtggccat gaagcccagc ctcatgttcc 660
tggccaaggc aggcagccgc gacatcgccg cctactgcaa ctacacgcag taccagcccc 720
gtgtgctggc tgtcatcggg cccactcgt cagagctcgc catggtcacc ggcaagttct 780
tcagcttctt cctcatgccc cagtggggcg cccccacca tcaccaccc ccaaccaacc 840
cctgccccgt gggagcccc tgtgtcagga gaatgctaca tgcacccac ccagccctgc 900
cctgggagcc ctgtgtcaga agatgctctt ggccttgag gtcagctacg gtgctagcat 960
ggagctgctg agcgcgggg agaccttccc ctcttcttc cgcaccgtgc ccagcgaccg 1020
tgtgcagctg acggccgcgc cggagctgct gcaggagtgc ggctggaact ggggtggccgc 1080
cctgggcagc gacgacgagt acggccggca gggcctgagc atcttctcgc ccctggccgc 1140
ggcacgcggc atctgcatcg cgcacgaggg cctggtgccg ctgccccgtg ccgatgactc 1200

```



gcggtctgggg	aaggtgcagg	acgtcctgca	ccaggtgaac	cagagcagcg	tgcaggtggt	1260
gctgctgttc	gcctccgtgc	acgccgccca	cgccctcttc	aactacagca	tcagcagcag	1320
gctctcgccc	aaggtgtggg	tggccagcga	ggcctggctg	acctctgacc	tggtcatggg	1380
gctgcccggc	atggcccaga	tgggcacggt	gcttggtctc	ctccagaggg	gtgccacgt	1440
gcacgagttc	ccccagtacg	tgaagacgca	cctggccctg	gccaccgacc	cggccttctg	1500
ctctgccctg	ggcagagagg	agcagggtct	ggaggaggac	gtggtggggc	agcgctgcc	1560
gcagtgtgac	tgcatacagg	tgcagaacgt	gagcgcaggg	ctaaatcacc	accagacgtt	1620
ctctgtctac	gcagctgtgt	atagcgtggc	ccaggccctg	cacaacactc	ttcagtgcaa	1680
cgctcaggc	tgccccgcgc	aggacccctg	gaagccctgg	caggtgagcc	cgggagatgg	1740
gggtgtgctg	tcctctgcat	gtgcccaggc	caccaggcac	ggccaccacg	cctgagctgg	1800
aggtggctgg	cggctcagcc	ccgtcccccg	cccgagctc	ctggagaaca	tgtacaacct	1860
gaccttccac	gtgggcgggc	tgccgctgcg	gttcgacagc	agcggaaacg	tggacatgga	1920
gtacgacctg	aagctgtggg	tgtggcaggg	ctcagtgccc	aggtccacag	acgtgggcag	1980
gttcaaccgc	agcctcagga	cagagcgctt	gaagatccgc	tggcacacgt	ctgacaacca	2040
ggtgaggtga	gggtgggtgt	gccaggcgtg	cccgtaggtg	cccccgcggc	agggcgcgagc	2100
ctgggggtgg	gggcccgttc	agtctcccgt	gggcatgccc	agccgagcag	agccagaccc	2160
caggcctgtg	cgcagaagcc	cgtgtcccgg	tgctcgcggc	agtgccagga	gggccaggtg	2220
cgccgggtca	aggggttcca	ctcctgctgc	tacgactgtg	tggactgcga	ggcgggcagc	2280
taccggcaac	accacgtga	gcccgcttcc	cggcaggctg	gggtgggaac	gcagcagggg	2340
aggtgcctgc	caagtctga	ctctgagacc	agagcccaca	gggtacaaga	cgaacacca	2400
gcgcccctct	cctctctcac	agacgacatc	gcctgcacct	tttgtggcca	ggatgagtgg	2460
tccccggagc	gaagcacacg	ctgcttcgcg	cgcaggtctc	ggttcctggc	atggggcgag	2520
ccggtgtgtc	tgctgtgtct	cctgtgtgtg	agcctggcgc	tgggccttgt	gctggctgct	2580
ttggggctgt	tcgttaccca	tcgggacagc	ccactggttc	aggcctcggg	ggggcccctg	2640
gcctgctttg	gcctggtgtg	cctgggcctg	gtctgcctca	gcgtcctcct	gttccttggc	2700
gcgccagcc	ctgcccgatg	cctggcccag	cagcccttgt	cccacctccc	gctcacgggc	2760
tcgctgagca	cactcttcct	cgaggcgcc	gagatcttcg	tggagtcaga	actgcctctg	2820
agctgggcag	accggtgtag	tggctgcctg	cgggggccct	gggcctggct	ggtggtgctg	2880
ctggccatgc	tggtaggagt	cgcactgtgc	acctggtacc	tggtagcctt	ccgcgccgag	2940
gtggtgacgg	actggcacat	gctgccacg	gaggcgctgg	tgcactgccg	cacacgtccc	3000
tgggtcagct	tcggcctagc	gcacgccacc	aatgccacgc	tggcctttct	ctgcttccctg	3060
ggcactttcc	tggtagcgag	ccagccgggc	tgtataaacc	gtgcccgtag	cctcaccttt	3120
gccatgctgg	ctacttcct	cacctgggtc	tcctttgtgc	cctcctggcg	caatgtgcag	3180
gtggtcctca	ggcccccgct	gcagatgggc	gccctcctgc	tctgtgtcct	gggctcctg	3240
gctgccttcc	acctgccag	gtgttacctg	ctcatgcggc	agccagggct	caacaccccc	3300
gagttcttcc	tgggaggggg	ccctggggat	gcccgaaggc	agaatgacgg	gaacacagga	3360
aatcagggga	aacatgagtg	acccaacctt	gtgatctcag	ccccggtgaa	cccagactta	3420
gctgcgatcc	ccccaaagcc	agcaatgacc	cgtgtctcgc	tacagagacc	ctcccgtctt	3480
aggttctgac	cccaggttgt	ctcctgacct	tgacccca	gtgagcccta	ggcctggagc	3540
acgtgacac	ccctgtgacc	atc				3563

```
<210> 21
<211> 839
<212> PRT
<213> Homo sapiens
```

```

<400> 21
Met Gly Pro Arg Ala Lys Thr Ile Cys Ser Leu Phe Phe Leu Leu Trp
  1             5             10             15

Val Leu Ala Glu Pro Ala Glu Asn Ser Asp Phe Tyr Leu Pro Gly Asp
      20             25             30

Tyr Leu Leu Gly Gly Leu Phe Ser Leu His Ala Asn Met Lys Gly Ile
      35             40             45

```

Val	His	Leu	Asn	Phe	Leu	Gln	Val	Pro	Met	Cys	Lys	Glu	Tyr	Glu	Val	50	55	60
Lys	Val	Ile	Gly	Tyr	Asn	Leu	Met	Gln	Ala	Met	Arg	Phe	Ala	Val	Glu	65	70	75
Glu	Ile	Asn	Asn	Asp	Ser	Ser	Leu	Leu	Pro	Gly	Val	Leu	Leu	Gly	Tyr	85	90	95
Glu	Ile	Val	Asp	Val	Cys	Tyr	Ile	Ser	Asn	Asn	Val	Gln	Pro	Val	Leu	100	105	110
Tyr	Phe	Leu	Ala	His	Glu	Asp	Asn	Leu	Leu	Pro	Ile	Gln	Glu	Asp	Tyr	115	120	125
Ser	Asn	Tyr	Ile	Ser	Arg	Val	Val	Ala	Val	Ile	Gly	Pro	Asp	Asn	Ser	130	135	140
Glu	Ser	Val	Met	Thr	Val	Ala	Asn	Phe	Leu	Ser	Leu	Phe	Leu	Leu	Pro	145	150	155
Gln	Ile	Thr	Tyr	Ser	Ala	Ile	Ser	Asp	Glu	Leu	Arg	Asp	Lys	Val	Arg	165	170	175
Phe	Pro	Ala	Leu	Leu	Arg	Thr	Thr	Pro	Ser	Ala	Asp	His	His	Val	Glu	180	185	190
Ala	Met	Val	Gln	Leu	Met	Leu	His	Phe	Arg	Trp	Asn	Trp	Ile	Ile	Val	195	200	205
Leu	Val	Ser	Ser	Asp	Thr	Tyr	Gly	Arg	Asp	Asn	Gly	Gln	Leu	Leu	Gly	210	215	220
Glu	Arg	Val	Ala	Arg	Arg	Asp	Ile	Cys	Ile	Ala	Phe	Gln	Glu	Thr	Leu	225	230	235
Pro	Thr	Leu	Gln	Pro	Asn	Gln	Asn	Met	Thr	Ser	Glu	Glu	Arg	Gln	Arg	245	250	255
Leu	Val	Thr	Ile	Val	Asp	Lys	Leu	Gln	Gln	Ser	Thr	Ala	Arg	Val	Val	260	265	270
Val	Val	Phe	Ser	Pro	Asp	Leu	Thr	Leu	Tyr	His	Phe	Phe	Asn	Glu	Val	275	280	285
Leu	Arg	Gln	Asn	Phe	Thr	Gly	Ala	Val	Trp	Ile	Ala	Ser	Glu	Ser	Trp	290	295	300
Ala	Ile	Asp	Pro	Val	Leu	His	Asn	Leu	Thr	Glu	Leu	Gly	His	Leu	Gly	305	310	315
Thr	Phe	Leu	Gly	Ile	Thr	Ile	Gln	Ser	Val	Pro	Ile	Pro	Gly	Phe	Ser	325	330	335
Glu	Phe	Arg	Glu	Trp	Gly	Pro	Gln	Ala	Gly	Pro	Pro	Pro	Leu	Ser	Arg	340	345	350

Thr	Ser	Gln	Ser	Tyr	Thr	Cys	Asn	Gln	Glu	Cys	Asp	Asn	Cys	Leu	Asn	355	360	365
Ala	Thr	Leu	Ser	Phe	Asn	Thr	Ile	Leu	Arg	Leu	Ser	Gly	Glu	Arg	Val	370	375	380
Val	Tyr	Ser	Val	Tyr	Ser	Ala	Val	Tyr	Ala	Val	Ala	His	Ala	Leu	His	385	390	395
Ser	Leu	Leu	Gly	Cys	Asp	Lys	Ser	Thr	Cys	Thr	Lys	Arg	Val	Val	Tyr	405	410	415
Pro	Trp	Gln	Leu	Leu	Glu	Glu	Ile	Trp	Lys	Val	Asn	Phe	Thr	Leu	Leu	420	425	430
Asp	His	Gln	Ile	Phe	Phe	Asp	Pro	Gln	Gly	Asp	Val	Ala	Leu	His	Leu	435	440	445
Glu	Ile	Val	Gln	Trp	Gln	Trp	Asp	Arg	Ser	Gln	Asn	Pro	Phe	Gln	Ser	450	455	460
Val	Ala	Ser	Tyr	Tyr	Pro	Leu	Gln	Arg	Gln	Leu	Lys	Asn	Ile	Gln	Asp	465	470	475
Ile	Ser	Trp	His	Thr	Val	Asn	Asn	Thr	Ile	Pro	Met	Ser	Met	Cys	Ser	485	490	495
Lys	Arg	Cys	Gln	Ser	Gly	Gln	Lys	Lys	Lys	Pro	Val	Gly	Ile	His	Val	500	505	510
Cys	Cys	Phe	Glu	Cys	Ile	Asp	Cys	Leu	Pro	Gly	Thr	Phe	Leu	Asn	His	515	520	525
Thr	Glu	Asp	Glu	Tyr	Glu	Cys	Gln	Ala	Cys	Pro	Asn	Asn	Glu	Trp	Ser	530	535	540
Tyr	Gln	Ser	Glu	Thr	Ser	Cys	Phe	Lys	Arg	Gln	Leu	Val	Phe	Leu	Glu	545	550	555
Trp	His	Glu	Ala	Pro	Thr	Ile	Ala	Val	Ala	Leu	Leu	Ala	Ala	Leu	Gly	565	570	575
Phe	Leu	Ser	Thr	Leu	Ala	Ile	Leu	Val	Ile	Phe	Trp	Arg	His	Phe	Gln	580	585	590
Thr	Pro	Ile	Val	Arg	Ser	Ala	Gly	Gly	Pro	Met	Cys	Phe	Leu	Met	Leu	595	600	605
Thr	Leu	Leu	Leu	Val	Ala	Tyr	Met	Val	Val	Pro	Val	Tyr	Val	Gly	Pro	610	615	620
Pro	Lys	Val	Ser	Thr	Cys	Leu	Cys	Arg	Gln	Ala	Leu	Phe	Pro	Leu	Cys	625	630	635
Phe	Thr	Ile	Cys	Ile	Ser	Cys	Ile	Ala	Val	Arg	Ser	Phe	Gln	Ile	Val	645	650	655

Cys Ala Phe Lys Met Ala Ser Arg Phe Pro Arg Ala Tyr Ser Tyr Trp  
                   660                  665                  670  
 Val Arg Tyr Gln Gly Pro Tyr Val Ser Met Ala Phe Ile Thr Val Leu  
                   675                  680                  685  
 Lys Met Val Ile Val Val Ile Gly Met Leu Ala Thr Gly Leu Ser Pro  
                   690                  695                  700  
 Thr Thr Arg Thr Asp Pro Asp Asp Pro Lys Ile Thr Ile Val Ser Cys  
                   705                  710                  715                  720  
 Asn Pro Asn Tyr Arg Asn Ser Leu Leu Phe Asn Thr Ser Leu Asp Leu  
                   725                  730                  735  
 Leu Leu Ser Val Val Gly Phe Ser Phe Ala Tyr Met Gly Lys Glu Leu  
                   740                  745                  750  
 Pro Thr Asn Tyr Asn Glu Ala Lys Phe Ile Thr Leu Ser Met Thr Phe  
                   755                  760                  765  
 Tyr Phe Thr Ser Ser Val Ser Leu Cys Thr Phe Met Ser Ala Tyr Ser  
                   770                  775                  780  
 Gly Val Leu Val Thr Ile Val Asp Leu Leu Val Thr Val Leu Asn Leu  
                   785                  790                  795                  800  
 Leu Ala Ile Ser Leu Gly Tyr Phe Gly Pro Lys Cys Tyr Met Ile Leu  
                   805                  810                  815  
 Phe Tyr Pro Glu Arg Asn Thr Pro Ala Tyr Phe Asn Ser Met Ile Gln  
                   820                  825                  830  
 Gly Tyr Thr Met Arg Arg Asp  
                   835

<210> 22  
 <211> 6  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
           PDZIP peptide sequence

<400> 22  
 Ser Val Ser Thr Val Val  
       1                  5

<210> 23  
 <211> 2520  
 <212> DNA  
 <213> Homo sapiens

<400> 23  
 atggggccca gggcaaagac catctgctcc ctgttcttcc tcctatgggt cctggctgag 60

```

ccggctgaga actcggactt ctacctgect ggggattacc tcctgggtgg cctcttctcc 120
ctccatgcca acatgaaggg cattgttcac cttaacttcc tgcaggtgcc catgtgcaag 180
gagtatgaag tgaagtgat aggctacaac ctcatgcagg ccatgcgctt cgcggtggag 240
gagatcaaca atgacagcag cctgctgcct ggtgtgctgc tgggctatga gatcgtggat 300
gtgtgttaca tctccaacaa tgtccagccg gtgctctact tcctggcaca cgaggacaac 360
ctccttccca tccaagagga ctacagtaac tacatttccc gtgtgggtggc tgtcattggc 420
cctgacaact ccgagtctgt catgactgtg gccaacttcc tctccctatt tctccttcca 480
cagatcacct acagcgccat cagcgatgag ctgcgagaca aggtgcgctt cccggctttg 540
ctgcgtagca caccagcgc cgaccaccac gtcgaggcca tgggtgcagct gatgctgcac 600
ttccgctgga actggatcat tgtgctgggtg agcagcgaca cctatggccg cgacaatggc 660
cagctgcttg gcgagcgcgt ggcccggcgc gacatctgca tcgccttcca ggagacgctg 720
cccacactgc agccaacca gaacatgacg tcagaggagc gccagcgcct ggtgaccatt 780
gtggacaagc tgcagcagag cacagcgcgc gtcgtggtcg tgttctcgcc cgacctgacc 840
ctgtaccact tcttcaatga ggtgctgcgc cagaacttca cgggcgcgct gtgctcgcc 900
tccgagtcct gggcatcga cccggtcctg cacaacctca cggagctggg ccaacttgggc 960
accttctctg gcatcacctat ccagagcgtg cccatcccgg gcttcagtga gttccgcgag 1020
tggggccccc aggtctggcc gccacccctc agcaggacca gccagagcta tacctgcaac 1080
caggagtgcg acaactgcct gaacgccacc ttgtccttca acaccattct caggctctct 1140
ggggagcgtg tcgtctacag cgtgtactct gcggtctatg ctgtggccca tgcctgcac 1200
agcctctctg gctgtgacaa aagcacctgc accaagaggg tggcttacc ctggcagctg 1260
cttgaggaga tctggaagg caacttcaat ctctggacc accaaatctt ctgcgaccg 1320
caaggggacg tggctctgca cttggagatt gtccagtggc aatgggaccg gagccagaat 1380
cccttccaga gcgtcgctc ctactacccc ctgcagcgac agctgaagaa catccaagac 1440
atctcctggc acaccgtcaa caacacgatc cctatgtcca tgtgttccaa gaggtgccag 1500
tcagggcaaaa agaagaagcc tgtgggcatc cacgtctgct gcttcgagtg catcgactgc 1560
cttcccggca ccttccctcaa ccacactgaa gatgaatatg aatgccaggc ctgcccgaat 1620
aacgagtggg cctaccagag tgagacctcc tgcttcaagc ggcagctggt cttcctggaa 1680
tggcatgagg caccacccat cgctgtggcc ctgctggcgc ccctgggctt cctcagcacc 1740
ctggccatcc tgggtgatatt ctggaggcac ttccagacac ccatagttcg ctcggtggg 1800
ggcccatgt gcttctctgat gctgacactg ctgctgggtg catacatggt ggtcccgtg 1860
tacgtggggc cgcccaaggc ctccacctgc ctctgccgcc aggcctctt tccctctgc 1920
ttcacaattt gcatctcctg tategcctg cgttctttcc agatcgtctg cgccttcaag 1980
atggccagcc gcttcccacg cgcctacagc tactgggtcc gctaccaggg gccctacgtc 2040
tctatggcat ttatcacggg actcaaaatg gtcattgtgg taattggcat gctggccacg 2100
ggcctcagtc ccaccaccg tactgacccc gatgacccca agatcacaat tgtctcctgt 2160
aaccccaact accgcaacag cctgctgttc aacaccagcc tggacctgct gctctcagt 2220
gtgggtttca gcttcgccta catgggcaaa gagctgccc ccaactacaa cgaggccaag 2280
ttcatcacc tcagcatgac cttctatttc acctcatccg tctccctctg caccttcatg 2340
totgcctaca gcgggtgtgt ggtcaccatc gtggacctct tggtcactgt gctcaacctc 2400
ctggccatca gcctgggcta cttcgcccc aagtgttaca tgatcctctt ctaccgggag 2460
cgcaacacgc ccgcctactt caacagcatg atccagggct acaccatgag gagggactag 2520

```

<210> 24

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Six-His tag

<400> 24

His His His His His His

1

5